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Patent

Attorney's Docket No. 012627-025

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of)

Prof. Dr. Hans SCHACKERT et al.)

Group Art Unit: Unassigned)

Application No.: Unassigned)
(Corresponding to PCT/EP00/02330)

Examiner: Unassigned)

International Filing Date: 16 March 2000)

For: METHOD FOR IDENTIFYING)
ORGANISMS BY MEANS OF)
COMPARATIVE GENETIC)
ANALYSIS AND PRIMERS AND)
HYBRIDISATION PROBES FOR)
CARRYING OUT THIS METHOD)**PRELIMINARY AMENDMENT**Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Prior to examination, kindly amend the above-identified application as follows:

IN THE CLAIMS:

Kindly replace claims 1-45 and 47-52 as follows:

1. (Amended) A method of identifying organisms by comparative genetic analysis, wherein the coding and/or non-coding areas and/or functionally significant areas of highly conserved genes and/or their homologous genes and/or their cDNA copies and/or their pseudogenes are amplified using PCR and are subsequently genotyped and analyzed.

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cont.

4. (Amended) The method according to claim 1, wherein either the sense strand or the antisense strand of any species DNA or also their PCR copies are used for the identification.

5. (Amended) The method according to claim 1, wherein animals are identified.

6. (Amended) The method according to claim 1, wherein vertebrates are identified.

7. (Amended) The method according to claim 1, wherein mammals are identified.

8. (Amended) The method according to claim 1, wherein plants are identified.

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9. (Amended) The method according to claim 1, wherein genotyping is carried out by DNA sequencing, any hybridization method, restriction fragment length analyses, chromatographic methods, spectroscopic and mass-spectroscopic methods, allele-specific PCR or by other methods suitable for detecting DNA sequence variants.

10. (Amended) The method according to claim 1, wherein exon and/or intron areas as well as functionally significant areas of the highly conserved tumor suppressor gene PTEN/MMAC1 and its homologues are used for amplification and subsequent genetic analysis.

11. (Amended) The method according to claim 1, wherein cDNA copies of the PTEN/MMAC1 gene and its homologues are used for the genetic analysis.

12. (Amended) The method according to claim 1, wherein pseudogenes or segments of pseudogenes of the PTEN/MMAC1 gene and its homologues are used for the genetic analysis.

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13. (Amended) The method according to claim 1, wherein exons arranged next to the PTEN/MMAC1 gene and its homologues and/or the parts of the introns following the exons are analyzed genetically.

14. (Amended) The method according to claim 1, wherein the exon regions 1 and 2 and/or 3 and 4 and/or 4 and 5 and/or 5 and 6 and/or 6 and 7 and/or 7 and 8 and/or 8 and 9 with the enclosed intron regions 1 and/or 2 and/or 3 and/or 4 and/or 5 and/or 6 and/or 7 and/or 8 as well as the 5'- and 3'-untranslated regions of the PTEN/MMAC1 gene and their homologues are used for the genetic analysis.

15. (Amended) The method according to claim 1, comprising selecting areas of highly conserved genes and/or pseudogenes and their homologues, constructing suitable oligonucleotides as primers which bind to the corresponding complementary coding and/or non-coding areas and/or functionally significant areas, amplifying them by means of a suitable technique and comparatively analyzing the sequence of the corresponding coding and/or non-coding area of various species by genetic analysis.

16. (Amended) The method according to claim 15, wherein areas of the PTEN/MMAC1 gene and/or the pseudogene and their homologues are selected.

17. (Amended) The method according to claim 15, wherein differing sequence segments of each individual exon, intron or untranslated region of the PTEN/MMAC1 gene and their homologues or the corresponding cDNA are selected.

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18. (Amended) The method according to claim 1, wherein genotyping of pig DNA which is obtained from foodstuffs, is carried out on the basis of the gene sequence variant of PTEN/MMAC1 containing a 9-base pair long deletion.

19. (Amended) An oligonucleotide primer for the PCR and the sequencing of exon 1 and/or 5'-untranslated region of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex1-401 sense

5'-cccttctactgcctcca -3'

PTENex1 -465 sense

5'- gggaggggggtctgagt -3'

PTENex1 ATG sense

5' - atgacagccatcatcaaaga -3'

PTENex1 R antisense

5' - aggtcaagtctaagtcgaatc -3'

20. (Amended) The oligonucleotide primer for PCR and the sequencing of exon
2 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex2F sense

5' - atatttatccaaacattattgctat -3'

PTENex2R antisense

5' - cttactacatcatcaatattgttcc -3'

21. (Amended) The oligonucleotide primer for PCR and the sequencing of exon
4, intron 4 and exon 5 of the PTEN/MMAC1 gene and its homologues, comprising the
following sequences:

Zoo43sUV sense

5' - tgtgctgagagacattatgac -3'

PTENex6R antisense

5'- gca agt tcc gcc act gaa -3'

24. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 7 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex7F sense

5'- cct cag ttt gtg gtc tgc ca -3'

PTENex7R antisense

5'- c ctt ttt tag cat ctt gtt ctg ttt -3'

25. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 8 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex8F sense

5'- caa aat gtt tca ctt ttg ggt aaa -3'

PTENex8R antisense

5'- taa aat ttg gag aaa agt atc ggt t -3'

26. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 9 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex9F sense

5'- gtg aag ctg tac ttc aca aaa ac -3'

PTENex9tga antisense

5'- aaa aaa att cag act ttt gta att tg -3'

27. (Amended) The method according to claim 1, wherein the DNA amplification involves a mixture of oligonucleotides which differ at the 3' region of the oligonucleotide as regards its length by one or more nucleotides or which differ as regards their nucleotide sequence at the 3' end of the oligonucleotide at one or more positions.

28. (Amended) The method according to claim 1, wherein the oligonucleotides

sense:

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat t -3',

antisense:

5' - cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc t -3'

are used for the amplification.

29. (Amended) The method according to claim 1, wherein the oligonucleotides
sense:

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gaa -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gag -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gat -3',

antisense:

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt a -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt g -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt t -3'

are used for the amplification.

30. (Amended) The method according to claim 1, wherein DNA sequencing
methods are used for the genetic analysis.

31. (Amended) The method according to claim 1, wherein DNA sequencing techniques are used in the genetic analysis for the PTEN/MMAC1 and/or its pseudogenes and their homologues.

32. (Amended) The method of distinguishing the DNA of various species, wherein at least one hybridization probe pair is used, the melting points of different combinations are determined and compiled for each species into a panel.

33. (Amended) The method of distinguishing the DNA of various species, wherein at least one hybridization probe pair is used and at least one gene segment is amplified, differing hybridization probe pairs hybridize to different gene segments, and the melting points of the different combinations are determined and compiled for each species into a panel and/or compared with this panel for the purpose of identification.

34. (Amended) The method of distinguishing the DNA of different species according to claim 33, wherein at least one hybridization probe pair is used and at least one gene segment of at least one species is amplified, differing hybridization probe pairs hybridize to different gene segments of various species, and the melting points of the different combinations are determined and compiled for each species into a panel and/or compared with this panel for the purpose of identification.

35. (Amended) The method of distinguishing the DNA of various species according to claim 33, wherein at least two hybridization probes of SEQ Nos. 3 to 8 are used, the melting points of different combinations are determined and compiled for each species into a panel.

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36. (Amended) The method according to claim 33, wherein the species differentiation of pig DNA from various other species is made using the hybridization probe pair A1/A2 as the hybridization probe pair.

37. (Amended) The method according to claim 33, wherein the hybridization probes are used in combinations C1/C2; A1/B2; A1/A2; C1/A2; B1/B2; B1/A2 for the species differentiation between various species.

38. (Amended) LightCycler hybridization probes for exon 5, comprising the sequences:

A1: 5'- tgc ata ttt gtt tca tcc ggg caa att -fluorescein -3'

A2: 5'- LC Red 705 - tta aag gca caa gat ttc tat ggg ga - ph -3'

B1: 5'- tgc ata ttt att aca tcg ggg caa att -fluorescein -3'

B2: 5'- LC Red 640 - aag gca caa gag gcc cta gat ttc ta - ph -3'

C1: 5'-tgc ata ttt gtt aca tcg ggg taa att fluorescein -3'

PTENex7L*640

5'-LC Red 640- acc cac acg acg gga aga caa g - ph -3'

PTENex7 FL

5'-ggtaacggctgagggaactcaaagtac - fluorescein -3'

PTENex7 LC (705-labeled)

5'-LC Red 705- tgaacttgcttcccgctcgtgtgg- ph -3'

41. (Amended) LightCycler hybridization probes for exon 8, comprising the following sequences

PTENex8F*

5'- tga caa gga ata tct agt act tac ttt aac aaa-fluorescein -3'

PTENex8L* 705

5'-LC Red 705 - ctt gac aaa gca aat aaa gac aaa gc- ph -3'

PTENex8 FLU

5' - tgctatcgatttcttgatcacatagacttccatttt - fluorescein -3'

PTENex8 LCR (640-labeled)

5'-LC Red 640- actttttctgaggtttctctggtcctggtat - ph -3'

42. (Amended) [The] LightCycler hybridization probes for exon 9, comprising the following sequences

PTENex9 FL

5'-aac atc tgg tgt tac aga agt tga act gct- fluorescein -3'

PTENex9 LC 640

5'-LC-640- cct ctg gat ttg acg gct cct cta ct - ph -3'

43. (Amended) Hybridization probe pair AI/A2: specific to PTEN pseudogene pig, comprising

AI
SEQ No. 3 A1: 5'- tgc ata ttt gtt tca tcc ggg caa att -fluorescein -3'

cont-7
SEQ No. 4 A2: 5'-LC Red 705- tta aag gca caa gat ttc tat ggg ga - ph -3'

44. (Amended) Hybridization probe pair B1/B2: specific to pseudogene man, comprising

SEQ No. 5 B1: 5'- tgc ata ttt att aca tcg ggg caa att -fluorescein -3'

SEQ No. 6 B2: 5'-LC Red 640- aag gca caa gag gcc cta gat ttc ta -ph -3'

45. (Amended) Hybridization probe pair C1/C2: specific to PTEN pseudogene man (C2) and homologue of pig (C1) comprising

SEQ No. 7 - C1: 5'- tgc ata ttt gtt aca tcg ggg taa att - fluorescein -3'

A1
cont
SEQ No. 8 - C2: corresponds to probe B2.

47. (Amended) DNA sequences of homologues of the PTEN/MMAC1 gene and/or of homologues of the PTEN/MMAC1 pseudogene, which are compiled in the annex under "list of species sequences", which as compared to the PTEN/MMAC1 gene and/or the PTEN/MMAC1 pseudogene comprise genetic variants comprising base substitutions and/or insertions and/or deletions and are suited for identifying corresponding species.

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48. (Amended) A kit for carrying out the method according to claim 1, comprising:

- a) one or more vessels comprising PCR and/or sequencing oligonucleotides binding to highly conserved genes, the oligonucleotides being optionally labeled radioactively or by means of a dye or in another way,
- b) vessels having further common reagents for DNA amplification and/or DNA analysis,

and

- c) a vessel containing a control DNA which is suited for testing the oligonucleotides and the reaction conditions.

49. (Amended) The kit according to claim 48, comprising:

- a) one or more vessels with PCR and/or sequencing oligonucleotides.

50. (Amended) The kit for identifying species for carrying out the method according to claim 1, comprising:

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- a) a vessel having an oligonucleotide pair comprising the following sequences:
 5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3' and 5'- cag
 gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',
 - b) two vessels with one of the following sequencing oligonucleotides each,
 these oligonucleotides being optionally labeled radioactively or by means of
 a dye or in another way:
 5'- cag gaa aca gct atg ac -3' and
 5'- cga cgt tgt aaa acg acg gcc agt -3',
 - c) a vessel containing a control *DNA*, which is suited for testing the
 oligonucleotides and the reaction conditions.

51. (Amended) The kit (Light Cycler Kit) for carrying out the method according
 to claim 32, comprising

- a) one or more vessels containing PCR primers and hybridization probes,
 which bind to highly conserved genes, the hybridization probes being
 optionally labeled by means of a dye,
 - b) vessels containing further common reagents for DNA amplification and/or
 DNA analysis,
- and

- A2
cont.
- c) a vessel containing a control DNA which is suited for testing the oligonucleotides and the reaction conditions.

52. (Amended) The kit (Light Cycler Kit) for carrying out the method according to claim 32, comprising:

- a) one or more vessels with PCR primers and hybridization probes.
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REMARKS

Entry of the foregoing amendments is respectfully requested.

Respectfully submitted,

BURNS, DOANE, SWECKER & MATHIS, L.L.P.

By: _____

Teresa Stanek Rea
Registration No. 30,427

P.O. Box 1404
Alexandria, Virginia 22313-1404
(703) 836-6620

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